

KW



PCT09

## RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/09/743,825

TIME: 07:58:02

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\02132002\I743825.raw

**ENTERED**

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4 <110> APPLICANT: Chuaqui, Rodrigo F.
5      Cole, Kristina A.
6      Liotta, Lance A.
9 <120> TITLE OF INVENTION: PB39, A Gene Dysregulated in Prostate
10     Cancer and Uses Thereof
13 <130> FILE REFERENCE: 66043 /US
15 <140> CURRENT APPLICATION NUMBER: 09/743,825
16 <141> CURRENT FILING DATE: 1999-07-23
18 <150> PRIOR APPLICATION NUMBER: US 60/094,137
19 <151> PRIOR FILING DATE: 1998-07-24
21 <150> PRIOR APPLICATION NUMBER: PCT/US99/16831
22 <151> PRIOR FILING DATE: 1999-07-23
24 <160> NUMBER OF SEQ ID NOS: 17
26 <170> SOFTWARE: FastSEQ for Windows Version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2326
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (77)...(1753)
37 <400> SEQUENCE: 1
38   ccggggctgg aggggggcaa gcggttccg aggtgcaaag cctggtgcc cgagccctgc      60
39   ggagctcggg gccagc atg gcc ccc acg ctg caa cag gcg tac cgg agg cgc      112
40           Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg
41           1           5           10
43   tgg tgg atg gcc tgc acg gct gtg ctg gag aac ctc ttc ttc tct gct      160
44   Trp Trp Met Ala Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala
45           15           20           25
47   gta ctc ctg ggc tgg ggc tcc ctg ttg atc att ctg aag aac gag ggc      208
48   Val Leu Leu Gly Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly
49           30           35           40
51   ttc tat tcc agc acg tgc cca gct gag agc agc aac acc acc cag      256
52   Phe Tyr Ser Ser Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln
53   45           50           55           60
55   gat gag cag cgc agg tgg cca ggc tgt gac cag cag gag atg ctc      304
56   Asp Glu Gln Arg Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu
57           65           70           75
59   aac ctg ggc ttc acc att ggt tcc ttc gtg ctc agc gcc acc acc ctg      352
60   Asn Leu Gly Phe Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu
61           80           85           90
63   cca ctg ggg atc ctc atg gac cgc ttt ggc ccc cga ccc gtg cgg ctg      400
64   Pro Leu Gly Ile Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu

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65	95	100	105	
67	gtt ggc agt gcc tgc ttc act gcg tcc tgc acc ctc atg gcc ctg gcc	448		
68	Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala			
69	110 115 120			
71	tcc cgg gac gtg gaa gct ctg tct ccg ttg ata ttc ctg gcg ctg tcc	496		
72	Ser Arg Asp Val Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser			
73	125 130 135 140			
75	ctg aat ggc ttt ggt ggc atc tgc cta acg ttc act tca ctc acg ctg	544		
76	Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu			
77	145 150 155			
79	ccc aac atg ttt ggg aac ctg cgc tcc acg tta atg gcc ctc atg att	592		
80	Pro Asn Met Phe Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile			
81	160 165 170			
83	ggc tct tac gcc tct tct gcc att acg ttc cca gga atc aag ctg atc	640		
84	Gly Ser Tyr Ala Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile			
85	175 180 185			
87	tac gat gcc ggt gtg gcc ttc gtg gtc atc atg ttc acc tgg tct ggc	688		
88	Tyr Asp Ala Gly Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly			
89	190 195 200			
91	ctg gcc tgc ctt atc ttt ctg aac tgc acc ctc aac tgg ccc atc gaa	736		
92	Leu Ala Cys Leu Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu			
93	205 210 215 220			
95	gcc ttt cct gcc cct gag gaa gtc aat tac acg aag aag atc aag ctg	784		
96	Ala Phe Pro Ala Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu			
97	225 230 235			
99	agt ggg ctg gcc ctg gac cac aag gtg aca ggt gac ctc ttc tac acc	832		
100	Ser Gly Leu Ala Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr			
101	240 245 250			
103	cat gtg acc acc atg ggc cag agg ctc agc cag aag gcc ccc agc ctg	880		
104	His Val Thr Thr Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu			
105	255 260 265			
107	gag gac ggt tgc gat gcc ttc atg tca ccc cag gat gtt cgg ggc acc	928		
108	Glu Asp Gly Ser Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr			
109	270 275 280			
111	tca gaa aac ctt cct gag agg tct gtc ccc tta cgc aag agc ctc tgc	976		
112	Ser Glu Asn Leu Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys			
113	285 290 295 300			
115	tcc ccc act ttc ctg tgg agc ctc ctc acc atg ggc atg acc cag ctg	1024		
116	Ser Pro Thr Phe Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu			
117	305 310 315			
119	cgg atc atc ttc tac atg gct gct gtg aac aag atg ctg gag tac ctt	1072		
120	Arg Ile Ile Phe Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu			
121	320 325 330			
123	gtg act ggt ggc cag gag cat gag aca aat gaa cag caa caa aag gtg	1120		
124	Val Thr Gly Gly Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val			
125	335 340 345			
127	gca gag aca gtt ggg ttc tac tcc tcc gtc ttc ggg gcc atg cag ctg	1168		
128	Ala Glu Thr Val Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu			
129	350 355 360			

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131  ttg tgc ctt ctc acc tgc ccc ctc att ggc tac atc atg gac tgg cgg      1216
132  Leu Cys Leu Leu Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg
133  365                               370                               380
135  atc aag gac tgc gtg gac gcc cca act cag ggc act gtc ctc gga gat      1264
136  Ile Lys Asp Cys Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp
137  385                               390                               395
139  gcc agg gac ggg gtt gct acc aaa tcc atc aga cca cgc tac tgc aag      1312
140  Ala Arg Asp Gly Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys
141  400                               405                               410
143  atc caa aag ctc acc aat gcc atc agt gcc ttc acc ctg acc aac ctg      1360
144  Ile Gln Lys Leu Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu
145  415                               420                               425
147  ctg ctt gtg ggt ttt ggc atc acc tgt ctc atc aac aac tta cac ctc      1408
148  Leu Leu Val Gly Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu
149  430                               435                               440
151  cag ttt gtg acc ttt gtc ctg cac acc att gtt cga ggt ttc ttc cac      1456
152  Gln Phe Val Thr Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His
153  445                               450                               455                               460
155  tca gcc tgt ggg agt ctc tat gct gca gtg ttc cca tcc aac cac ttt      1504
156  Ser Ala Cys Gly Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe
157  465                               470                               475
159  ggg acg ctg aca ggc ctg cag tcc ctc atc agt gct gtg ttc gcc ttg      1552
160  Gly Thr Leu Thr Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu
161  480                               485                               490
163  ctt cag cag cca ctt ttc atg gcg atg gtg gga ccc ctg aaa gga gag      1600
164  Leu Gln Gln Pro Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu
165  495                               500                               505
167  ccc ttc tgg gtg aat ctg ggc ctc ctg cta ttc tca ctc ctg gga ttc      1648
168  Pro Phe Trp Val Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe
169  510                               515                               520
171  ctg ttg cct tcc tac ctc ttc tat tac cgt gcc cgg ctc cag cag gag      1696
172  Leu Leu Pro Ser Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu
173  525                               530                               535                               540
175  tac gcc gcc aat ggg atg ggc cca ctg aag gtg ctt agc ggc tct gag      1744
176  Tyr Ala Ala Asn Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu
177  545                               550                               555
179  gtg acc gca tagacttctc agaccaaggg acctggatga caggcaatca      1793
180  Val Thr Ala
183  aggctgagc aacaaaaagg agtgcccat atggcttttc tacctgtaac atgcacatag      1853
184  agccatggcc gtagatttat aaataccaag agaagttcta tttttgtaaa gactgcaaaa      1913
185  aggaggaaaa aaaaccttca aaaacgcccc ctaagtcaac gctccattga ctgaagacag      1973
186  tccctatcct agaggggttg agctttcttc ctccctgggt tggaggagac caggggtgct      2033
187  cttatctcct tctagcgtgc tgccctctgg tacctcttgg ggggatcggc aaacaggcta      2093
188  cccctgaggt cccatgtgcc atgagtgtgc acaacatgca atgtgtctgt gtatgtgtga      2153
189  atgtgagaaa aacacagccc tcctttcaga aggaaagggg cctgaggtgc cagctgtgtc      2213
190  ctgggttagg ggttgggggt cggcccttc cagggccagg aaggcaggtt ccctctctgg      2273
191  tgctgctgct tgcaagtctt agaggaaata aaaaggggaag tgagaaaaaa aaa      2326
193 <210> SEQ ID NO: 2
194 <211> LENGTH: 559

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195 <212> TYPE: PRT
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 2
199 Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg Trp Trp Met Ala
200 1 5 10 15
201 Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala Val Leu Gly
202 20 25 30
203 Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly Phe Tyr Ser Ser
204 35 40 45
205 Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln Asp Glu Gln Arg
206 50 55 60
207 Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu Asn Leu Gly Phe
208 65 70 75 80
209 Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu Pro Leu Gly Ile
210 85 90 95
211 Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu Val Gly Ser Ala
212 100 105 110
213 Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala Ser Arg Asp Val
214 115 120 125
215 Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser Leu Asn Gly Phe
216 130 135 140
217 Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu Pro Asn Met Phe
218 145 150 155 160
219 Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile Gly Ser Tyr Ala
220 165 170 175
221 Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile Tyr Asp Ala Gly
222 180 185 190
223 Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly Leu Ala Cys Leu
224 195 200 205
225 Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu Ala Phe Pro Ala
226 210 215 220
227 Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu Ser Gly Leu Ala
228 225 230 235 240
229 Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr His Val Thr Thr
230 245 250 255
231 Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu Glu Asp Gly Ser
232 260 265 270
233 Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr Ser Glu Asn Leu
234 275 280 285
235 Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys Ser Pro Thr Phe
236 290 295 300
237 Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu Arg Ile Ile Phe
238 305 310 315 320
239 Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu Val Thr Gly Gly
240 325 330 335
241 Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val Ala Glu Thr Val
242 340 345 350
243 Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu Leu Cys Leu Leu
244 355 360 365

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245 Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg Ile Lys Asp Cys
246      370      375      380
247 Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp Ala Arg Asp Gly
248      385      390      395      400
249 Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys Ile Gln Lys Leu
250      405      410      415
251 Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu Leu Leu Val Gly
252      420      425      430
253 Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu Gln Phe Val Thr
254      435      440      445
255 Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His Ser Ala Cys Gly
256      450      455      460
257 Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe Gly Thr Leu Thr
258      465      470      475      480
259 Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu Leu Gln Gln Pro
260      485      490      495
261 Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu Pro Phe Trp Val
262      500      505      510
263 Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe Leu Leu Pro Ser
264      515      520      525
265 Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu Tyr Ala Ala Asn
266      530      535      540
267 Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu Val Thr Ala
268      545      550      555

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270 &lt;210&gt; SEQ ID NO: 3

271 &lt;211&gt; LENGTH: 3442

272 &lt;212&gt; TYPE: DNA

273 &lt;213&gt; ORGANISM: Homo sapiens

275 &lt;220&gt; FEATURE:

276 &lt;221&gt; NAME/KEY: CDS

277 &lt;222&gt; LOCATION: (1760)...(3439)

279 &lt;400&gt; SEQUENCE: 3

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282 ggccctgcacg gctgtgctgg agaacctctt cttctctgct gtactcctgg gctggggctc      180
283 cctgttgatc attctgaaga acgagggtt ctattccagc acgtgccag ctgagagcag      240
284 caccaacacc acccaggatg agcagcgag gtggccaggc tgtgaccagc aggacgagat      300
285 gctcaacctg ggcttcacca ttggttcctt cgtgctcagc gccaccacc tgccactggg      360
286 gatcctcatg gaccgctttg gccccgacc cgtgcggtg gttggcagt cctgcttcac      420
287 tgcgtcctgc accctcatgg ccttggcctc ccgggacgtg gaagctctgt ctccgttgat      480
288 attcctggcg ctgtccctga atggttttgg tggcatctgc ctaacgttca cttcactcac      540
289 gctgcccac atgtttggga acctgcgctc cacgttaatg gccctcatga ttggctctta      600
290 cgctctttct gccattacgt tccaggaat caagctgac tacgatgccg gtgtggcctt      660
291 cgtggtcatc atgttcacct ggtctggcct ggcctgcctt atctttctga actgcaccct      720
292 caactggccc atcgaagcct ttctgcccc tgagggaagtc aattacacga agaagatcaa      780
293 gctgagtggg ctggccctgg accacaaggt gacaggtgac ctcttctaca cccatgtgac      840
294 caccatgggc cagaggctca gccagaaggc cccagcctg gaggacggtt cggatgcctt      900
295 catgtcacc caggatgttc ggggcacctc agaaaacctt cctgagaggt ctgtccctt      960
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VERIFICATION SUMMARY

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